

## GEPHE SUMMARY

	Gephebase Gene		GepheID
Dihydropteroate synthase (pvdhps) ( <a href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase+Dihydropteroate+synthase+(pvdhps)^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase+Dihydropteroate+synthase+(pvdhps)^#gephebase-summary-title</a> )		GP00001485	
Published	Entry Status	Prigent	Main curator

## PHENOTYPIC CHANGE

	Trait Category	
Physiology ( <a href="https://www.gephebase.org/search-criteria?/and+Trait+Category+Physiology^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Trait+Category+Physiology^#gephebase-summary-title</a> )		
	Trait	
Xenobiotic resistance (sulfadoxine) ( <a href="https://www.gephebase.org/search-criteria?/and+Trait+Xenobiotic+resistance+(sulfadoxine)^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Trait+Xenobiotic+resistance+(sulfadoxine)^#gephebase-summary-title</a> )		
	Trait State in Taxon A	
Malaria parasite - sensitive		
	Trait State in Taxon B	
Malaria parasite - resistant		
	Ancestral State	
Unknown		
	Taxonomic Status	
Intraspecific ( <a href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status+Intraspecific^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status+Intraspecific^#gephebase-summary-title</a> )		

Taxon A	Latin Name	Taxon B	Latin Name
Plasmodium vivax ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms+Plasmodium+vivax^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms+Plasmodium+vivax^#gephebase-summary-title</a> )		Plasmodium vivax ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms+Plasmodium+vivax^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms+Plasmodium+vivax^#gephebase-summary-title</a> )	
	Common Name		Common Name
malaria parasite P. vivax		malaria parasite P. vivax	
	Synonyms		Synonyms
Haemamoeba vivax; malaria parasite P. vivax		Haemamoeba vivax; malaria parasite P. vivax	
	Rank		Rank
species		species	
	Lineage		Lineage
cellular organisms; Eukaryota; Alveolata; Apicomplexa; Aconoidasida; Haemosporida; Plasmodiidae; Plasmodium; Plasmodium (Plasmodium)		cellular organisms; Eukaryota; Alveolata; Apicomplexa; Aconoidasida; Haemosporida; Plasmodiidae; Plasmodium; Plasmodium (Plasmodium)	
	Parent		Parent
Plasmodium (Plasmodium) () - (Rank: subgenus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=418103">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=418103</a> )		Plasmodium (Plasmodium) () - (Rank: subgenus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=418103">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=418103</a> )	
	NCBI Taxonomy ID		NCBI Taxonomy ID
5855 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=5855">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=5855</a> )		5855 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=5855">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=5855</a> )	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		No	

## GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Plasmodium vivax
DHPS		Q00LX9 ( <a href="http://www.uniprot.org/uniprot/Q00LX9">http://www.uniprot.org/uniprot/Q00LX9</a> )	
	Synonyms		GenebankID or UniProtKB
-		JN794522.1 ( <a href="https://www.ncbi.nlm.nih.gov/nuccore/JN794522.1">https://www.ncbi.nlm.nih.gov/nuccore/JN794522.1</a> )	
	String		
-			
	Sequence Similarities		
-			
	GO - Molecular Function		
GO:0004156 : dihydropteroate synthase activity ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0004156">https://www.ebi.ac.uk/QuickGO/term/GO:0004156</a> )			
	GO - Biological Process		
GO:0042558 : pteridine-containing compound metabolic process ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0042558">https://www.ebi.ac.uk/QuickGO/term/GO:0042558</a> )			
	GO - Cellular Component		
-			
			Presumptive Null
Unknown ( <a href="https://www.gephebase.org/search-criteria?/and+Presumptive+Null+Unknown^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Presumptive+Null+Unknown^#gephebase-summary-title</a> )			
			Molecular Type
Unknown ( <a href="https://www.gephebase.org/search-criteria?/and+Molecular+Type+Unknown^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Molecular+Type+Unknown^#gephebase-summary-title</a> )			

Unknown (<https://www.gephebase.org/search-criteria?/and+Aberration+Type=^Unknown^#gephebase-summary-title>)

Molecular Details of the Mutation

unknown

Experimental Evidence

Association Mapping (<https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=^Association+Mapping^#gephebase-summary-title>)

Main Reference

Genomic analysis of local variation and recent evolution in *Plasmodium vivax*. (2016) (<https://pubmed.ncbi.nlm.nih.gov/27348299>)

Authors

Pearson RD; Amato R; Auburn S; Miotto O; Almagro-Garcia J; Amaratunga C; Suon S; Mao S; Noviyanti R; Trimarsanto H; Marfurt J; Anstey NM; William T; Boni MF; Dolecek C; Hien TT; White NJ; Michon P; Siba P; Tavul L; Harrison G; Barry A; Mueller I; Ferreira MU; Karunaweera N; Randrianarivelosia M; Gao Q; Hubbart C; Hart L; Jeffery B; Drury E; Mead D; Kekre M; Campino S; Manske M; Cornelius VJ; MacInnis B; Rockett KA; Miles A; Rayner JC; Fairhurst RM; Nosten F; Price RN; Kwiatkowski DP

Abstract

The widespread distribution and relapsing nature of *Plasmodium vivax* infection present major challenges for the elimination of malaria. To characterize the genetic diversity of this parasite in individual infections and across the population, we performed deep genome sequencing of >200 clinical samples collected across the Asia-Pacific region and analyzed data on >300,000 SNPs and nine regions of the genome with large copy number variations. Individual infections showed complex patterns of genetic structure, with variation not only in the number of dominant clones but also in their level of relatedness and inbreeding. At the population level, we observed strong signals of recent evolutionary selection both in known drug resistance genes and at new loci, and these varied markedly between geographical locations. These findings demonstrate a dynamic landscape of local evolutionary adaptation in the parasite population and provide a foundation for genomic surveillance to guide effective strategies for control and elimination of *P. vivax*.

Additional References

## RELATED GEPHE

Related Genes

5 (ABC transporter pvmp1, Dihydrofolate reductase (pvdhfr), Multidrug resistance protein 1 (pvmdr1), PVX\_084940, PVX\_101445) (<https://www.gephebase.org/search-criteria?/or+Taxon+ID=^5855^/and+Trait=Xenobiotic+resistance/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

## EXTERNAL LINKS

## COMMENTS

With strong evidence of recent selection in western Thailand. The signal of selection encompasses multiple genes such that we cannot be certain of the specific gene under selection. A noteworthy candidate also observed in selective sweeps in South America